



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Caput, Daniel
Ferrara, Pascual
Laurent, Patrick
Vita, Natalio

(ii) TITLE OF INVENTION: IL-13 receptor

(iii) NUMBER OF SEQUENCES: 4

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1539 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (F) TISSUE TYPE: Carcinoma
- (G) CELL TYPE: renal
- (H) CELL LINE: caki-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGTGCCTGTC	GGCGGGGAGA	GAGGCAATAT	CAAGGTTTTA	AATCTGGAG	AAATGGCTTA	60	
ATT CGTTTG	C	TG GCT ATCG	GAT GCT TATA	TAC CTTTCTG	ATA AGCACAA	CATT GGCTG	120
TACAAGCTTT	TGC ACTTCAT	CTTCAGACAC	CGACATAAAA	GTTAACCCCTC	CTCAGGATT		180
TGAGATAGTG	GATTATGAAG	AGAACCCGGA	TACTTAGGTT	ATCTCTATTT	GCAATGGCAA		240
CCCCCACTGT	CTCTGGATCA	TTTGTGTTG	TGAAGGAAT	GCACAGTGG	ATATGAAC	TA	300
AAATACCGAA	ACATTGGTAG	TGAAACATGG	AAGGCTAGTG	TAGAGGTTAC	CATCATTACT		360
AAGAATCTAC	ATTACAAAGA	TGGGTTTGAT	CTTAACAAGG	GCATTGAATT	ATAGAAGGGC		420
GAAGATAACAC	ACGCTTTAC	CATGGCAATG	CACAAATGGA	TCAGAAGTTC	AAAGTTCCAA		480
TTGCTAGGAG	TGGGCAGAAA	CTACTTATTG	GATATCACCA	CAAGGAATTC	CAGAAACTAA		540
AGTTCA	GAGGAT	TAAGTTTG	GTAGAATGGA	TTGCGTATAT	TACAATTGGC	AATATTTACT	600
CTGTTCTTG	AAACCTGGCA	TAGGTTACAT	TATGTCTGGG	TACTTCTTGA	TACCAATTAC		660
AACTTCTTT	ACTGGTATGA	GGGCTTGGAT	CATGCATTAA	ATATATTGG	AAACAGTGTG		720

TTGATTACAT CAAGGCTGAT GGACAAAATA TAGGATGCAG ATTCCTAT TTGGCAATAA 780
AGGAGCAGTG AGGCATCAGA CTATAAAGAT TTCTATATT GTGTTAATGG ATCATCAGAG 840
AACAAAGCCTG AAATATCAAG GAATCAGATC CAGTTATTTC ACTTTTCAGC TTCAAAATAT 900
AGTTAACCT TTGCCGCCAG TCAGTTGGAA ATATCTTACT TTTACTCGGG AGAGTTCATG 960
TGAAATTAAG CTGAAATGGA GCATACCTTT GTTAGGCCTT GGACCTATT CAGCAAGGTG 1020
TTTGATTAT GAAATTGAGA TCAGAGAAGA TGATACTACC GAAAGCATGG AGGAATTTG 1080
GTGACTGCTA CAGTTGAAAA TGAAACATAC ACCTTGAAAA CAACAAATGA AACCCGAATA 1140
ATAGAGTTT TAGTAGCAAT TATGCTTGT AGTAAGAACG AAAGTGAATA TTTATTGCTC 1200
AGATGACGGA ATTTGGCAA AGAATCAAGT AGTGAGTGG GTGATAAACAA ATGCTGGAA 1260
GGTGAAGACC TATCGAAGAA AACTTGCTA GTAGCTGGGA TCGTTCTGG CTACCATTG 1320
GTTTCATCTT AATATTAGTT ATATTGTAA CCGGTCTGCT TAGTGAATGT TGCCTAAAGCC 1380
AAACACCTAC CCAAAATGA TTCCAGAATT TTTCTGTGAT ACATGAAGAA GATTTGCATC 1440
TTTCCATATC AAGAGACATG GTATTGACTC AACAGTTCC AGTCATGGCC AAATGTTCAA 1500
TATGAGTCTC AATAAACTGA ATTTTCTTG CGAATGTTG 1539

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 380 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens
(F) TISSUE TYPE: Carcinoma
(G) CELL TYPE: renal
(H) CELL LINE: Caki-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ala Phe Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile
1 5 10 15

Ser Thr Thr Phe Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val
20 25 30

Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr
35 40 45

Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu
50 55 60

Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr
65 70 75 80

Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp

85

90

95

Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln
100 105 110

Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr
115 120 125

Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp
130 135 140

Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly
145 150 155 160

Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu
165 170 175

Gly Leu Asp His Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly
180 185 190

Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys
195 200 205

Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg
210 215 220

Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro
225 230 235 240

Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu
245 250 255

Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr
260 265 270

Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val
275 280 285

Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu
290 295 300

Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly
305 310 315 320

Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu
325 330 335

Ser Lys Lys Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu
340 345 350

Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr
355 360 365

Tyr Pro Lys Met Ile Pro Glu Phe Phe Cys Asp Thr
370 375 380

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4009 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens
(F) TISSUE TYPE: Carcinoma
(G) CELL TYPE: RENAL
(H) CELL LINE: Caki-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TCAGCCCCGGC CGGGCTCCGA GGCGAGAGGC TGCATGGAGT GGCCGGCGCG GCTCTGCGGG 60
CTGTGGCGC TGCTGCTCTG CGCCGGCGGC GGGGGCGGGG GCAGGGCGC CGCGCCTACG 120
GAAACTCAGC CACCTGTGAC AAATTTGAGT GTCTCTGTTG AAAACCTCTG CACAGTAATA 180
TGGACATGGA ATCCACCCGA GGGAGCCAGC TCAAATTGTA GTCTATGGTA TTTTAGTCAT 240
TTTGGCGACA AACAAAGATAA GAAAATAGCT CCGGAAACTC GTCGTTCAAT AGAAGTACCC 300
CTGAATGAGA GGATTTGTCT GCAAGTGGGG TCCCAGTGTG GCACCAATGA GAGTGAGAAG 360
CCTAGCATTT TGGTTGAAAA ATGCATCTCA CCCCCAGAAG GTGATCCTGA GTCTGCTGTG 420
ACTGAGCTTC AATGCATTTG GCACAACCTG AGCTACATGA AGTGTCTTG GCTCCCTGGA 480
AGGAATACCA GTCCCGACAC TAACTATACT CTCTACTATT GGCACAGAAG CCTGGAAAAA 540
ATTCCATCAAT GTGAAAACAT CTTTAGAGAA GGCCAATACT TTGGTTGTTG CTTTGATCTG 600
ACCAAAGTGA AGGATTCCAG TTTGAACAA CACAGTGTCC AAATAATGGT CAAGGATAAT 660
GCAGGAAAAA TTAAACCATC CTTCAATATA GTGCCTTAA CTTCCCGTGT GAAACCTGAT 720
CCTCCACATA TTAAAAACCT CTCCTTCCAC AATGATGACC TATATGTGCA ATGGGAGAAT 780
CCACAGAATT TTATTAGCAG ATGCCTATT TATGAAGTAG AAGTCAATAA CAGCCAAACT 840
GAGACACATA ATGTTTCTA CGTCCAAGAG GCTAAATGTG AGAATCCAGA ATTTGAGAGA 900
AATGTGGAGA ATACATCTTG TTTCATGGTC CCTGGTGTTC TTCCTGATAC TTTGAACACA 960
GTCAGAATAA GAGTCAAAAC AAATAAGTTA TGCTATGAGG ATGACAAACT CTGGAGTAAT 1020
TGGAGCCAAG AAATGAGTAT AGGTAAGAAG CGCAATTCCA CACTCTACAT AACCATGTTA 1080
CTCATTGTTG CAGTCATCGT CGCAGGTGCA ATCATAGTAC TCCTGCTTAA CCTAAAAAGG 1140
CTCAAGATTA TTATATTCCC TCCAATTCCCT GATCCTGGCA AGATTTTAA AGAAATGTTT 1200
GGAGACCAGA ATGATGATAC TCTGCACTGG AAGAAGTAGG ACATCTATGA GAAGCAAACC 1260
AAGGAGGAAA CCGACTCTGT AGTGCTGATA GAAAACCTGA AGAAAGCCTC TCAGTGATGG 1320

AGATAATTAA TTTTACCTT CACTGTGACC TTGAGAAGAT TCTTCCCATT CTCCATTGT 1380
TATCTGGAA CTTATTAAAT GGAAACTGAA ACTACTGCAC CATTAAAAAA CAGGCAGCTC 1440
ATAAGAGCCA CAGGTCTTTA TGTTGAGTCG CGCACCGAAA AACTAAAAAT AATGGGCCT 1500
TTGGAGAAGA GTGTGGAGTC ATTCTCATTG AATTATAAAA GCCAGCAGGC TTCAAACTAG 1560
GGGACAAAGC AAAAAGTGAT GATAGTGGTG GAGTTAATCT TATCAAGAGT TGTGACAAC 1620
TCCTGAGGGA TCTATACATTG CTTTGTGTT CTTGTGTCAA CATGAACAAA TTTTATTGT 1680
AGGGGAACTC ATTTGGGGTG CAAATGCTAA TGTCAAACTT GAGTCACAAA GAACATGTAG 1740
AAAACAAAAT GGATAAAAATC TGATATGTAT TGTTTGGGAT CCTATTGAAC CATGTTGTG 1800
GCTATTAAA CTCTTTAAC AGTCTGGCT GGGTCCGGTG GCTCACGCCT GTAATCCCAG 1860
CAATTGGGA GTCCGAGGCG GGCAGATCAC TCGAGGTCAG GAGTTCCAGA CCAGCCTGAC 1920
CAAATGGTG AAACCTCCTC TCTACTAAAA CTACAAAAAT TAACTGGGTG TGGTGGCGCG 1980
TGCCTGTAAT CCCAGCTACT CGGGAAAGCTG AGGCAGGTGA ATTGTTGAA CCTGGGAGGT 2040
GGAGGTTGCA GTGAGCAGAG ATCACACCCAC TGCACTCTAG CCTGGGTGAC AGAGCAAGAC 2100
TCTGTCTAAA AAACAAAACA AAACAAAACA AAACAAAAAA ACCTCTTAAT ATTCTGGAGT 2160
CATCATTCCC TTCGACAGCA TTTTCCTCTG CTTGAAAGC CCCAGAAATC AGTGTGGCC 2220
ATGATGACAA CTACAGAAAA ACCAGAGGCA GCTTCTTGC CAAGACCTTT CAAAGCCATT 2280
TTAGGCTGTT AGGGGCAGTG GAGGTAGAAT GACTCCTTGG GTATTAGAGT TTCAACCATG 2340
AAGTCTCTAA CAATGTATT TCTTCACCTC TGCTACTCAA GTAGCATTAA CTGTGTCTTT 2400
GGTTTGTGCT AGGCCCGG GTGTGAAGCA CAGACCCCTT CCAGGGTTT ACAGTCTATT 2460
TGAGACTCCT CAGTTCTTGC CACTTTTTT TTTAATCTCC ACCAGTCATT TTTCAGACCT 2520
TTTAACTCCT CAATTCCAAC ACTGATTCC CCTTTGCAT TCTCCCTCCT TCCCTTCCTT 2580
GTAGCCTTT GACTTCATT GGAAATTAGG ATGTAATCT GCTCAGGAGA CCTGGAGGAG 2640
CAGAGGATAA TTAGCATCTC AGGTTAAGTG TGAGTAATCT GAGAAACAAT GACTAATTCT 2700
TGCATATTAA GTAACTTCCA TGTGAGGGTT TTCAGCATTG ATATTGTGC ATTTCTAAA 2760
CAGAGATGAG GTGGTATCTT CACGTAGAAC ATTGGTATTC GCTTGAGAAA AAAAGAATAG 2820
TTGAACCTAT TTCTCTTCT TTACAAGATG GGTCCAGGAT TCCTCTTTC TCTGCCATAA 2880
ATGATTAATT AAATAGCTTT TGTGTCTTAC ATTGGTAGCC AGCCAGCCAA GGCTCTGTT 2940
ATGCTTTGG GGGGCATATA TTGGGTTCCA TTCTCACCTA TCCACACAAAC ATATCCGTAT 3000
ATATCCCCTC TACTCTTACT TCCCCAAAT TTAAAGAAGT ATGGGAAATG AGAGGCATTT 3060
CCCCCACCCC ATTTCTCTCC TCACACACAG ACTCATATTA CTGGTAGGAA CTTGAGAACT 3120
TTATTCCAA GTGTTCAAA CATTACCAA TCATATTAAT ACAATGATGC TATTGCAAT 3180

TCCTGCTCCT AGGGGAGGGG AGATAAGAAA CCCTCACTCT CTACAGGTTT GGGTACAAGT 3240
GGCAACCTGC TTCCATGGCC GTGTAGAACG ATGGTGCCCT GGCTTCTCTG AGGAAGCTGG 3300
GGTCATGAC AATGGCAGAT GTAAAGTTAT TCTTGAAGTC AGATTGAGGC TGGGAGACAG 3360
CCGTAGTAGA TGTTCTACTT TGTTCTGCTG TTCTCTAGAA AGAATATTTG GTTTCTGT 3420
ATAGGAATGA GATTAATTCC TTTCCAGGTA TTTTATAATT CTGGGAAGCA AAACCCATGC 3480
CTCCCCCTAG CCATTTTAC TGTTATCCTA TTTAGATGGC CATGAAGAGG ATGCTGTGAA 3540
ATTCCCAACA AACATTGATG CTGACAGTCA TGCAGTCTGG GAGTGGGAA GTGATCTTT 3600
GTTCCCATCC TCTTCTTTA GCAGTAAAAT AGCTGAGGGA AAAGGGAGGG AAAAGGAAGT 3660
TATGGGAATA CCTGTGGTGG TTGTGATCCC TAGGTCTTGG GAGCTCTTGG AGGTGTCTGT 3720
ATCAGTGGAT TTCCCATCCC CTGTGGAAA TTAGTAGGCT CATTACTGT TTTAGGTCTA 3780
GCCTATGTGG ATTTCCTTAA AACATACCTA AGCAAACCCA GTGTCAGGAT GGTAATTCTT 3840
ATTCTTCGT TCAGTTAAGT TTTCCCTTC ATCTGGCAC TGAAGGGATA TGTGAAACAA 3900
TGTTAACATT TTTGGTAGTC TTCAACCAGG GATTGTTCT GTTTAACTTC TTATAGGAAA 3960
GCTTGAGTAA AATAAATATT GTCTTTGT ATGTCACCCCA AAAAAAAA 4009

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 427 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens
(F) TISSUE TYPE: Carcinoma
(G) CELL TYPE: renal
(H) CELL LINE: Caki-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Glu Trp Pro Ala Arg Leu Cys Gly Leu Trp Ala Leu Leu Cys
1 5 10 15

Ala Gly Gly Gly Gly Gly Gly Ala Ala Pro Thr Glu Thr Gln
20 25 30

Pro Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val
35 40 45

Ile Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu
50 55 60

Trp Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro
65 70 75 80

Glu Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu
85 90 95

Gln Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile
100 105 110

Leu Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala
115 120 125

Val Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys
130 135 140

Ser Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu
145 150 155 160

Tyr Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile
165 170 175

Phe Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val
180 185 190

Lys Asp Ser Ser Phe Glu Gln His Ser Val Gln Ile Met Val Lys Asp
195 200 205

Asn Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser
210 215 220

Arg Val Lys Pro Asp Pro Pro His Ile Lys Asn Leu Ser Phe His Asn
225 230 235 240

Asp Asp Leu Tyr Val Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg
245 250 255

Cys Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln Thr Glu Thr His
260 265 270

Asn Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu
275 280 285

Arg Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro
290 295 300

Asp Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys
305 310 315 320

Tyr Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile
325 330 335

Gly Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met Leu Leu Ile Val
340 345 350

Pro Val Ile Val Ala Gly Ala Ile Ile Val Leu Leu Tyr Leu Lys
355 360 365

Arg Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile
370 375 380

Phe Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys
385 390 395 400

Lys Tyr Asp Ile Tyr Glu Lys Gln Thr Lys Glu Glu Thr Asp Ser Val
405 410 415

Val Leu Ile Glu Asn Leu Lys Lys Ala Ser Gln
420 425